

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 14

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2261 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 49..1551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

09072014 11:15:00

CGCAGCACGG CAACACATAC ACAGGAGCCA CACACCGCAC CTACCCCG ATG GAC GTC 5 Met Asp Val	57
CTC CTC CTG GAG AAG GCC CTC CTG GGC CTC TTC GCC GCG GCG GTG CTG Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala Ala Val Leu 5 10 15	105
GCC ATC GCC GTC GCC AAG CTC ACC GGC AAG CGC TTC CGC CTC CCC CCT Ala Ile Ala Val Ala Lys Leu Thr Gly Lys Arg Phe Arg Leu Pro Pro 20 25 30 35	153
GGC CCC TCC GGC GCC CCC ATC GTC GGC AAC TGG CTG CAG GTC GGC GAC Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln Val Gly Asp 40 45 50	201
GAC CTC AAC CAC CGC AAC CTG ATG GGC CTG GCC AAG CGG TTC GGC GAG Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg Phe Gly Glu 55 60 65	249
GTG TTC CTC CTC CGC ATG GGC GTC CGC AAC CTG GTG GTC GTC TCC ACC Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val Val Ser Ser 70 75 80	297
CCC GAG CTC GCC AAG GAG GTC CTC CAC ACC CAG GGC GTC GAG TTC GGC Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val Glu Phe Gly 85 90 95	345
TCC CGC ACC CGC AAC GTC GTC TTC GAC ATC TTC ACC GGC AAG GGA CAG Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly Lys Gly Gln 100 105 110 115	393
GAC ATG GTG TTC ACG GTG TAC GGC GAC CAC TGG CGC AAG ATG CGG CGG Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys Met Arg Arg 120 125 130	441
ATC ATG ACG GTG CCC TTC ACC AAC AAG GTG GTG GCG CAG AAC CGC Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala Gln Asn Arg 135 140 145	489
GTG GGG TGG GAG GAG GAG GCC CGG CTG GTG GTG GAG GAC CTC AAG GCC Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp Leu Lys Ala 150 155 160	537

03713797 112500

GAC CCG CCG GCG ACG GCG GGC GTG GTG GTC CGC CGC AGG CTG CAG Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg Arg Leu Gln 165 170 175	585
CTC ATG ATG TAC AAC GAC ATG TTC CGC ATC ATG TTC GAC CGC CGG TTC Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp Arg Arg Phe 180 185 190 195	633
GAG AGC GTG GCC GAC CCG CTC TTC AAC CAG CTC AAG GCG CTC AAC GCC Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala Leu Asn Ala 200 205 210	681
GAG CGC AGC ATC CTC TCC CAG AGC TTC GAC TAC AAC TAC GGC GAC TTC Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr Gly Asp Phe 215 220 225	729
ATC CCC GTC CTC CGC CCC TTC CTC CGC CGC TAC CTC AAC CGC TGC ACC Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn Arg Cys Thr 230 235 240	777
AAC CTC AAG ACC AAG CGG ATG AAG GTG TTC GAG GAC CAC TTC GTC CAG Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His Phe Val Gln 245 250 255	825
CAG CGC AAG GAG GCG TTG GAG AAG ACG GGT GAG ATC AGG TGC GCC ATG Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg Cys Ala Met 260 265 270 275	873
GAC CAC ATC CTG GAA GCC GAA AGG AAG GGC GAG ATC AAC CAC GAC AAC Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn His Asp Asn 280 285 290	921
GTC CTC TAC ATC GTC GAG AAC ATC AAC GTC GCA GCC ATC GAG ACG ACG Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile Glu Thr Thr 295 300 305	969
CTG TGG TCG ATC GAG TGG GGC CTC GCG GAG CTG GTG AAC CAC CCG GAG Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn His Pro Glu 310 315 320	1017
ATC CAG CAG AAG CTG CGC GAG GAG ATC GTC GCC GTT CTG GCC GGC GGC Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu Gly Ala Gly 325 330 335	1065
GTG GCG GTG ACG GAG CCG GAC CTG GAG CGC CTC CCC TAC CTG CAG TCC Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr Leu Gln Ser 340 345 350 355	1113
GTG GTG AAG GAG ACG CTC CGC CTC CGC ATG GCA ATC CCG CTC CTG GTG Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro Leu Leu Val 360 365 370	1161
CCG CAC ATG AAC CTC AGC GAC GCC AAG CTC GCC GGC TAC GAC ATC CCC Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr Asp Ile Pro 375 380 385	1209
GCC GAG TCC AAG ATC CTC GTC AAC GGC TGG TTC CTC GCC AAC GAC CCC Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala Asn Asp Pro 390 395 400	1257
AAG CGG TGG GTG CGC GCC GAT GAG TTC AGG CCG GAG AGG TTC CTC GAG Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg Phe Leu Glu 405 410 415	1305
GAG GAG AAG GCC GTC GAG GCC CAC GGC AAC GAT TTC CGG TTC GTG CCC Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg Phe Val Pro 420 425 430 435	1353

09/19/94 - 3:15:00

TTC GGC GTC GGC CGC CGG AGC TGC CCC GGG ATC ATC CTC GCG CTG CCC Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu Ala Leu Pro 440 445 450	1401
ATC ATC GGC ATC ACG CTC GGA CGC CTG GTG CAG AAC TTC CAG CTG CTG Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe Gln Leu Leu 455 460 465	1449
CCG CGG CGG GGG CAG GAC AAG ATC GAC ACC ACC GAG AAG CCC GGG CAG Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys Pro Gly Gln 470 475 480	1497
TTT ACC AAC CAG ATC CTC AAG CAC GCC ACC ATT GTC TGC AAG CCA CTC Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys Lys Pro Leu 485 490 495	1545
GAG GCT TAACTGAATT GAGGTTTCGG TCATGGGCACGC CCGCTGACGC GGGGAGATGG Glu Ala 500	1601
ATCTATGCAT GTGACTGTGT ATTTTGCTT CTTTCTTTTT GGTGTTGTTT TTTGCAGTAG TAAGTTTAAT TTTTCTTTGG TGTTGGCCTA TTTGTCTTCA TGTGAGGCCT CGTGTGTTAA ATTTCCATAT AGTTGGCAAT GTGATGTAAA ACTTGGCTCC AAAAAAAA AAAAAAAACT CGAGACTCTT CTCTCTCTCT AGCCTCGGGT CTCTGCTGGC AAGGAACTT GCATTACCCCT GTGTACGACG GCGCCATGTT CGTCCCTGAA GCACCCCTCCC TGCAGAGCTC CCAGGACAAC TTGCTGCTGCAT CTGCTGGTT CAAGCGTCGA AGGAGAGAGT TTTGAATACC CGAAAGAATA TAGCGTTGGA CATACTGTC AAACAGGGGA TCTTGCTGTG GGTCTCTTGG TGGGCAAAT CGCATAGACA ATCATTCAA TGGATGGTT CTTGCTGGT CGGTCAAAAA GTATATGTG TAATTGTACG CCTTTTTGG GTCTTGTGCAAAAGATCAT GGTATTGAG TTGTGAGCTC TGAGATAACA GGTTTGTGTA TAGTGAATAA AAGAGGAGCG TCGTCAACAC CATGTACTAT ATAGGCTTTG AAATTCCATT AAGATGCATC AGAAATCAAT GTTGGATTG 2261	1661 1721 1781 1841 1901 1961 2021 2081 2141 2201

09743754 111500

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATATATGGAT CCATGGACGT CCTCCTCCTG GAGAAGGC

38

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATATATGGAT CCATGGATGT TTTGTTGTTG GAGAAGGCC TCCTGGGCCT CTTCGC

56

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

DOCUMENT EDITION 2000

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATATATGGAT CCATGGATGT TTTGTTGTTG GAAAAAGCTT TGTTGGGTTT GTTCGCCGCG 60
GCGGTGCTGG C 71

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATATATGGAT CCATGGATGT TTTGTTGTTG GAAAAAGCTT TGTTGGGTTT GTTGCTGCT 60
GCTGTTTGG CTATTGCTGT TGCTAAATTG ACTGGTAAAA GATTTAGATT GCCACCAGGT 120
CCATCCGGCG CCCCCATCGT CGG 143

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

05/14/2014 10:45 AM

TATATAGAAT TCCAGTTAAG CCTCGAGTGG CTTGCAGAC

39

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

00737500

ATG GAT GTT TTG TTG GAG AAG GCC CTC CTG GCC CTC TTC GCC GCG Met Asp Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala 1 5 10 15	48
GCG GTG CTG GCC ATC GCC GTC GCC AAG CTC ACC GGC AAG CGC TTC CGC Ala Val Leu Ala Ile Ala Val Ala Lys Leu Thr Gly Lys Arg Phe Arg 20 25 30	96
CTC CCC CCT GGC CCC TCC GGC GCC CCC ATC GTC GGC AAC TGG CTG CAG Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln 35 40 45	144
GTC GGC GAC CTC AAC CAC CGC AAC CTC ATG GGC CTG GCC AAG CGG Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg 50 55 60	192
TTC GGC GAG GTG TTC CTC CTC CGC ATG GGC GTC CGC AAC CTG GTG GTC Phe Gly Glu Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val 65 70 75 80	240
GTC TCC AGC CCC GAG CTC GCC AAG GAG GTC CTC CAC ACC CAG GGC GTC Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val 85 90 95	288
GAG TTC GGC TCC CGC ACC CGC AAC GTC GTC TTC GAC ATC TTC ACC GGC Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly 100 105 110	336
AAG GGA CAG GAC ATG GTG TTC ACG GTG TAC GGC GAC CAC TGG CGC AAG Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys 115 120 125	384
ATG CGG CGG ATC ATG ACG GTG CCC TTC ACC AAC AAG GTG GTG GCG Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala 130 135 140	432
CAG AAC CGC GTG GGG TGG GAG GAG GAG GCC CGG CTG GTG GTG GAG GAC Gln Asn Arg Val Gly Trp Glu Glu Ala Arg Leu Val Val Glu Asp 145 150 155 160	480
CTC AAG GCC GAC CCG CGG CGG ACG CGG GGC GTG GTC GTC CGC CGC Leu Lys Ala Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg 165 170 175	528
AGG CTG CAG CTC ATG ATG TAC AAC GAC ATG TTC CGC ATC ATG TTC GAC Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp 180 185 190	576
CGC CGG TTC GAG AGC GTG GCC GAC CCG CTC TTC AAC CAG CTC AAG GCG Arg Arg Phe Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala 195 200 205	624
CTC AAC GCC GAG CGC AGC ATC CTC TCC CAG AGC TTC GAC TAC AAC TAC Leu Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr 210 215 220	672
GGC GAC TTC ATC CCC GTC CTC CGC CCC TTC CTC CGC CGC TAC CTC AAC Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn 225 230 235 240	720

09749444-11115000

CCG TGC ACC AAC CTC AAG ACC AAG CGG ATG AAG GTG TTC GAG GAC CAC Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His 245 250 255	768
TTC GTC CAG CAG CGC AAG GAG GCG TTG GAG AAG ACG GGT GAG ATC AGG Phe Val Gln Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg 260 265 270	816
TGC GCC ATG GAC CAC ATC CTG GAA GCC GAA AGG AAG GGC GAG ATC AAC Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn 275 280 285	864
CAC GAC AAC GTC CTC TAC ATC GTC GAG AAC ATC AAC GTC GCA GCC ATC His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile 290 295 300	912
GAG ACG ACG CTG TCG ATC GAG TGG GCC CTC GCG GAG CTG GTG AAC Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn 305 310 315 320	960
CAC CCG GAG ATC CAG CAG AAG CTG CGC GAG GAG ATC GTC GCC GTT CTG His Pro Glu Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu 325 330 335	1008
GGC GCC GGC GTG GCG GTG ACG GAG CCG GAC CTG GAG CGC CTC CCC TAC Gly Ala Gly Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr 340 345 350	1056
CTG CAG TCC GTG GTG AAG GAG ACG CTC CGC CTC CGC ATG GCA ATC CCG Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro 355 360 365	1104
CTC CTG GTG CCG CAC ATG AAC CTC AGC GAC GCC AAG CTC GCC GGC TAC Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr 370 375 380	1152
GAC ATC CCC GCC GAG TCC AAG ATC CTC GTC AAC GCC TGG TTC CTC GCC Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala 385 390 395 400	1200
AAC GAC CCC AAG CGG TGG GTG CGC GCC GAT GAG TTC AGG CCG GAG AGG Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg 405 410 415	1248
TTC CTC GAG GAG AAG GCC GTC GAG GCC CAC GGC AAC GAT TTC CGG Phe Leu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg 420 425 430	1296
TTC GTG CCC TTC GGC GTC CGC CGG AGC TGC CCC GGG ATC ATC CTC Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu 435 440 445	1344
GCG CTG CCC ATC ATC GGC ATC ACG CTC GGA CGC CTG GTG CAG AAC TTC Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe 450 455 460	1392
CAG CTG CTG CCG CCG GGG CAG GAC AAG ATC GAC ACC ACC GAG AAG Gln Leu Leu Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys 465 470 475 480	1440
CCC GGG CAG TTT ACC AAC CAG ATC CTC AAG CAC GCC ACC ATT GTC TGC Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys 485 490 495	1488
AAG CCA CTC GAG GCT TAA Lys Pro Leu Glu Ala 500	1506

DRAFT 2/2000

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATG GAT GTT TTG TTG GAA AAA GCT TTG TTG GGT TTG TTC GCC GCG Met Asp Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala 1 5 10 15	48
GCG GTG CTC GCC ATC GCC GTC GCC AAG CTC ACC GGC AAG CGC TTC CGC Ala Val Leu Ala Ile Ala Val Ala Lys Leu Thr Gly Lys Arg Phe Arg 20 25 30	96
CTC CCC CCT GGC CCC TCC GGC GCC CCC ATC GTC GGC AAC TGG CTG CAG Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln 35 40 45	144
GTC GGC GAC GAC CTC AAC CAC CGC AAC CTG ATG GGC CTG GCC AAG CGG Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg 50 55 60	192
TTC GGC GAG GTG TTC CTC CGC ATG GGC GTC CGC AAC CTG GTG GTC Phe Gly Glu Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val 65 70 75 80	240
GTC TCC AGC CCC GAG CTC GCC AAG GAG GTC CTC CAC ACC CAG GGC GTC Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val 85 90 95	288
GAG TTC GGC TCC CGC ACC CGC AAC GTC GTC TTC GAC ATC TTC ACC GGC Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly 100 105 110	336
AAG GGA CAG GAC ATG GTG TTC ACG GTG TAC GGC GAC CAC TGG CGC AAG Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys 115 120 125	384
ATG CGG CGG ATC ATG ACC GTG CCC TTC TTC ACC AAC AAG GTG GTG GCG Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala 130 135 140	432
CAG AAC CGC GTG GGG TGG GAG GAG GAG GCC CGG CTG GTG GTG GAG GAC Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp 145 150 155 160	480
CTC AAG GCC GAC CCG GCG GCG ACG GCG GGC GTG GTG GTG GTC CGC CGC Leu Lys Ala Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg 165 170 175	528
AGG CTG CAG CTC ATG ATG TAC AAC GAC ATG TTC CGC ATC ATG TTC GAC Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp 180 185 190	576
CGC CGG TTC GAG AGC GTG GCC GAC CCG CTC TTC AAC CAG CTC AAG GCG Arg Arg Phe Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala 195 200 205	624

0932794-112500

CTC AAC GCC GAG CGC AGC ATC CTC TCC CAG AGC TTC GAC TAC AAC TAC Leu Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr 210 215 220	672
GGC GAC TTC ATC CCC GTC CTC CGC CCC TTC CTC CGC CGC TAC CTC AAC Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn 225 230 235 240	720
CGC TGC ACC AAC CTC AAG ACC AAG CGG ATG AAG GTG TTC GAG GAC CAC Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His 245 250 255	768
TTC GTC CAG CAG CGC AAG GAG GCG TTG GAG AAG ACG GGT GAG ATC ACG Phe Val Gln Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg 260 265 270	816
TGC GCC ATG GAC CAC ATC CTG GAA GCC GAA AGG AAG GGC GAG ATC AAC Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn 275 280 285	864
CAC GAC AAC GTC CTC TAC ATC GTC GAG AAC ATC AAC GTC GCA GCC ATC His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile 290 295 300	912
GAG ACG ACG CTG TGG TCG ATC GAG TGG GGC CTC GCG GAG CTG GTG AAC Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn 305 310 315 320	960
CAC CCG GAG ATC CAG CAG AAG CTG CGC GAG GAG ATC GTC GCC GTT CTG His Pro Glu Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu 325 330 335	1008
GGC GCC GGC GTG GCG GTG ACG GAG CCG GAC CTG GAG CGC CTC CCC TAC Gly Ala Gly Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr 340 345 350	1056
CTG CAG TCC GTG GTG AAG GAG ACG CTC CGC CTC CGC ATG GCA ATC CCG Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro 355 360 365	1104
CTC CTG GTG CCG CAC ATG AAC AGC GAC GCC AAG CTC GGC GGC TAC Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr 370 375 380	1152
GAC ATC CCC GCC GAG TCC AAG ATC CTC GTC AAC GCC TGG TTC CTC GCC Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala 385 390 395 400	1200
AAC GAC CCC AAG CGG TGG GTG CGC GCC GAT GAG TTC AGG CCG GAG AGG Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg 405 410 415	1248
TTC CTC GAG GAG AAG GCC GTC GAG GCC CAC GGC AAC GAT TTC CGG Phe Leu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg 420 425 430	1296
TTC GTG CCC TTC GGC GTC CGC CGC AGC TGC CCC GGG ATC ATC CTC Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu 435 440 445	1344
GGC CTG CCC ATC ATC GGC ATC ACG CTC CGA CGC CTG GTG CAG AAC TTC Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe 450 455 460	1392
CAG CTG CTG CCG CGG GGG CAG GAC AAG ATC GAC ACC ACC GAG AAG Gln Leu Leu Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys 465 470 475 480	1440

CCC GGG CAG TTT ACC AAC CAG ATC CTC AAG CAC GCC ACC ATT GTC TGC	1488
Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys	
485	490
AAG CCA CTC GAG GCT TAA	1506
Lys Pro Leu Glu Ala	
500	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CDS 1..1503

ATG GAT GTT TTG TTG TTG GAA AAA GCT TTG TTG GGT TTG TTT GCT GCT Met Asp Val Leu Leu Leu Lys Ala Leu Leu Gly Leu Phe Ala Ala 505 510 515	48
GCT GTT TTG GCT ATT GCT GTT GCT AAA TTG ACT GGT AAA AGA TTT AGA Ala Val Leu Ala Ile Ala Val Ala Lys Leu Thr Gly Lys Arg Phe Arg 520 525 530	96
TTG CCA CCA GGT CCA TCC GGC GCC CCC ATC GTC GGC AAC TGG CTG CAG Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Thr Leu Gln 35 40 45	144
GTC GGC GAC GAC CTC AAC CAC CGC AAC CTG ATG GGC CTG GCC AAG CGG Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg 50 55 60	192
TTC GGC GAG GTG TTC CTC CTC CGC ATG GGC GTC CGC AAC CTG GTG GTC Phe Gly Glu Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val 65 70 75 80	240
GTC TCC AGC CCC GAG CTC GCC AAG GAG GTC CTC CAC ACC CAG GGC GTC Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val 85 90 95	288
GAG TTC GGC TCC CGC ACC CGC AAC GTC GTC TTC GAC ATC TTC ACC GGC Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly 100 105 110	336
AAG GGA CAG GAC ATG GTG TTC ACG GTG TAC GGC GAC CAC TGG CGC AAG Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys 115 120 125	384
ATG CGG CGG ATC ATG ACG GTG CCC TTC TTC ACC AAC AAG GTG GTG GCG Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala 130 135 140	432
CAG AAC CGC GTG GGG TGG GAG GAG GAG GCC CGG CTG GTG GTG GAG GAC Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp 145 150 155 160	480
CTC AAG GCC GAC CCG GCG GCG GCG ACG GCG GGC GTG GTG GTC CGC CGC Leu Lys Ala Asp Pro Ala Ala Thr Ala Gly Val Val Val Arg Arg 165 170 175	528

AGG CTG CAG CTC ATG ATG TAC AAC GAC ATG TTC CGC ATC ATG TTC GAC Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp 180 185 190	576
CGC CGG TTC GAG ACC GTG GCC GAC CCG CTC TTC AAC CAG CTC AAG GCG Arg Arg Phe Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala 195 200 205	624
CTC AAC GCC GAG CGC AGC ATC CTC TCC CAG ACC TTC GAC TAC AAC TAC Leu Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr 210 215 220	672
GGC GAC TTC ATC CCC GTC CTC CGC CCC TTC CTC CGC CGC TAC CTC AAC Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn 225 230 235 240	720
CGC TGC ACC AAC CTC AAG ACC AAG CGG ATG AAC GTC TTC GAG GAC CAC Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His 245 250 255	768
TTC GTC CAG CAG CGC AAG GAG GCG TTG GAG AAG ACG GGT GAG ATC AGG Phe Val Gln Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg 260 265 270	815
TGC GCC ATG GAC CAC ATC CTG GAA GCC GAA AGG AAG GGC GAG ATC AAC Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn 275 280 285	864
CAC GAC AAC GTC CTC TAC ATC GTC GAG AAC ATC AAC GTC GCA GCC ATC His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile 290 295 300	912
GAG ACG ACG CTG TGG TCG ATC GAG TGG GGC CTC GCG GAG CTG GTG AAC Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn 305 310 315 320	960
CAC CCG GAG ATC CAG CAG AAG CTG CGC GAG GAG ATC GTC GCC GTT CTG His Pro Glu Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu 325 330 335	1008
GGC GCC GGC GTG GCG GTG ACG GAG CCG GAC CTG GAG CGC CTC CCC TAC Gly Ala Gly Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr 340 345 350	1056
CTG CAG TCC GTG GTG AAG GAG ACG CTC CGC CTC CGC ATG GCA ATC CCG Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro 355 360 365	1104
CTC CTG GTG CCG CAC ATG AAC CTC AGC GAC GCC AAG CTC GCC GGC TAC Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr 370 375 380	1152
GAC ATC CCC GCC GAG TCC AAG ATC CTC GTC AAC GCC TGG TTC CTC GCC Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala 385 390 395 400	1200
AAC GAC CCC AAG CGG TGG GTG CGC GCG GAT GAG TTC AGG CCG GAG AGG Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg 405 410 415	1248
TTC CTC GAG GAG AAG GCG GTC GAG GCC CAC GGC AAC GAT TTC CGG Phe Leu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg 420 425 430	1296
TTC GTG CCC TTC GGC GTC GGC CGC CGG AGC TGC CCC GGG ATC ATC CTC Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu 435 440 445	1344

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GGC CTG CCC ATC ATC GGC ATC ACG CTC GGA CGC CTG GTG CAG AAC TTC Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe 450 455 460	1392
CAG CTG CTG CCG CCG GGG CAG GAC AAG ATC GAC ACC ACC GAG AAG Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys 465 470 475 480	1440
CCC GGG CAG TTT ACC AAC CAG ATC CTC AAG CAC GCC ACC ATT GTC TGC Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys 485 490 495	1488
AAG CCA CTC GAG GCT TAA Lys Pro Leu Glu Ala 500	1506

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(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2181 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 112..1734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGATCCACCC CTTGGATCCA CTCTACCCAG CTCGCTAGCC AGCGGGGTAC ATACACGCAC	60
GCACGTACGC GCGTACGTAC ACTCGCAGAG CTTGCTTCAG GGAGGCCGGC A ATG GAG	117
Met Glu	
1	
GTG GGG ACG TGG GCG GTG GTG TCG GCG GTG GCC GCG TAC ATG GCG	165
Val Gly Thr Trp Ala Val Val Val Ser Ala Val Ala Ala Tyr Met Ala	
5 10 15	
TGG TTC TGG CGG ATG TCC CGC GGG CTG CGC GGG CCG CGG GTT TGG CCC	213
Trp Phe Trp Arg Met Ser Arg Gly Leu Arg Gly Pro Arg Val Trp Pro	
20 25 30	
GTG CTC GGC AGC CTG CCG GGC CTG GTG CAG CAC GCC GAG GAC ATG CAC	261
Val Leu Gly Ser Leu Pro Gly Leu Val Gln His Ala Glu Asp Met His	
35 40 45 50	
GAG TGG ATC GCC GGC AAC CTG CGC CGC GCG GGC ACG TAC CAG ACC	309
Glu Trp Ile Ala Gly Asn Leu Arg Arg Ala Gly Gly Thr Tyr Gln Thr	
55 60 65	
TGC ATC TTC GCC GTG CCC GGG GTG GCG CGC CGC GGC CTG GTC ACC	357
Cys Ile Phe Ala Val Pro Gly Val Ala Arg Arg Gly Leu Val Thr	
70 75 80	
GTC ACC TGC GAC CCG CGC AAC CTG GAG CAC GTC CTG AAG GCG CGC TTC	405
Val Thr Cys Asp Pro Arg Asn Leu Glu His Val Leu Lys Ala Arg Phe	
85 90 95	
GAC AAC TAC CCC AAG GGC CCC TTC TGG CAC GGC GTC TTC CGG GAC CTG	453
Asp Asn Tyr Pro Lys Gly Pro Phe Trp His Gly Val Phe Arg Asp Leu	
100 105 110	

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CTC GGC GAC GGC ATC TTC AAT TCC GAC GGC GAC ACC TGG CTC GCG CAG Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Leu Ala Gln 115 120 125 130	501
CGC AAG ACG GCC GCG CTC GAG TTC ACC ACC CGC ACG CTC CGG ACG GCC Arg Lys Thr Ala Ala Leu Phe Thr Thr Arg Thr Leu Arg Thr Ala 135 140 145	549
ATG TCC CGC TGG GTC TCG CGC TCC ATC CAC GGC CGC CTC CTG CCC ATC Met Ser Arg Trp Val Ser Arg Ser Ile His Gly Arg Leu Leu Pro Ile 150 155 160	597
CTG GCC GAC GCG GCC AAG GGC AAG GCG CAG GTG GAT CTC CAG GAC CTC Leu Ala Asp Ala Ala Lys Gly Lys Ala Gln Val Asp Leu Gln Asp Leu 165 170 175	645
CTC CTC CGC CTC ACC TTC GAC AAC ATC TGC GGC CTG GCC TTC GGC AAG Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Ala Phe Gly Lys 180 185 190	693
GAC CCG GAG ACG CTC GCC CAG GGC CTG CCG GAG AAC GAG TTC GCC TCC Asp Pro Glu Thr Leu Ala Gln Gly Leu Pro Glu Asn Glu Phe Ala Ser 195 200 205 210	741
GCG TTC GAC CGC GCC ACC GAG GCC ACG CTC AAC CGC TTC ATC TTC CCG Ala Phe Asp Arg Ala Thr Glu Ala Thr Leu Asn Arg Phe Ile Phe Pro 215 220 225	789
GAG TTC CTG TGG CGC TGC AAA AAG TGG CTG GGC CTC GGC ATG GAG ACC Glu Phe Leu Trp Arg Cys Lys Lys Trp Leu Gly Leu Gly Met Glu Thr 230 235 240	837
ACG CTG ACC AGC AGC ATG GCC CAC GTC GAC CAG TAC CTC GCC GCC GTC Thr Leu Thr Ser Ser Met Ala His Val Asp Gln Tyr Leu Ala Ala Val 245 250 255	885
ATC AAG AAG CGC AAG CTC GAG CTC GCC GCC GGC AAC GGC AAA TGC GAC Ile Lys Lys Arg Lys Leu Glu Leu Ala Ala Gly Asn Gly Lys Cys Asp 260 265 270	933
ACG GCG GCG ACG CAC GAC GAC CTG CTC TCC CGG TTC ATG CGG AAG GGT Thr Ala Ala Thr His Asp Asp Leu Leu Ser Arg Phe Met Arg Lys Gly 275 280 285 290	981
TCC TAC TCG GAC GAG TCG CTC CAG CAC GTG GCG CTC AAC TTC ATC CTC Ser Tyr Ser Asp Glu Ser Leu Gln His Val Ala Leu Asn Phe Ile Leu 295 300 305	1029
GCC GGC CGC GAC ACC TCC TCC GTG GCG CTC TCC TGG TTC TTC TGG CTC Ala Gly Arg Asp Thr Ser Ser Val Ala Leu Ser Trp Phe Phe Trp Leu 310 315 320	1077
GTG TCC ACC CCT GCG GTG GAG CGC AAG ATC GTG CGC GAG CTC TGC TGC Val Ser Thr His Pro Ala Val Glu Arg Lys Ile Val Arg Glu Leu Cys 325 330 335	1125
TCC GTT CTC GCC GCG TCA CGG GGC GCC CAT GAC CGG GCA TTG TGG CTC Ser Val Leu Ala Ala Ser Arg Gly Ala His Asp Pro Ala Leu Trp Leu 340 345 350	1173
GCG GAG CCC TTC ACC TTC GAG GAG CTC GAC CGC CTG GTC TAC CTC AAG Ala Glu Pro Phe Thr Phe Glu Glu Leu Asp Arg Leu Val Tyr Leu Lys 355 360 365 370	1221
GCG GCG CTG TCG GAG ACC CTC CGC CTC TAC CCC TCC GTC CCC GAG GAC Ala Ala Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Glu Asp 375 380 385	1269

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TCC AAG CAC GTC GTC GCG GAC GAC TAC CTC CCC GAC GGC ACC TTC GTG Ser Lys His Val Val Ala Asp Asp Tyr Leu Pro Asp Gly Thr Phe Val 390 395 400	1317
CCG GCC GGG TCG TCG GTC ACC TAC TCC ATA TAC TCG GCG GGG CGC ATG Pro Ala Gly Ser Ser Val Thr Tyr Ser Ile Tyr Ser Ala Gly Arg Met 405 410 415	1365
AAG GGG GTG TGG GGG GAG GAC TGC CTC GAG TTC CCG CCG GAG CGA TGG Lys Gly Val Trp Gly Glu Asp Cys Leu Glu Phe Arg Pro Glu Arg Trp 420 425 430	1413
CTG TCG GCC GAC GGC ACC AAG TTC GAG CAG CAC GAC TCG TAC AAG TTC Leu Ser Ala Asp Gly Thr Lys Phe Glu Gln His Asp Ser Tyr Lys Phe 435 440 445 450	1461
GTG GCG TTC AAC GCC GGG CCG AGG GTG TGC CTG GGC AAG GAC CTA GCC Val Ala Phe Asn Ala Gly Pro Arg Val Cys Leu Gly Lys Asp Leu Ala 455 460 465	1509
TAC CTG CAG ATG AAG AAC ATC GCC GGG AGC GTG CTG CTC CGG CAC CGC Tyr Leu Gln Met Lys Asn Ile Ala Gly Ser Val Leu Leu Arg His Arg 470 475 480	1557
CTG ACC GTG GCG CCG GGC CAC CGC GTG GAG CAG AAG ATG TCG CTC ACG Leu Thr Val Ala Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr 485 490 495	1605
CTC TTC ATG AAG GGC GGG CTA CGG ATG GAG GTA CGT CCG CGC GAC CTC Leu Phe Met Lys Gly Gly Leu Arg Met Glu Val Arg Pro Arg Asp Leu 500 505 510	1653
GCC CCC GTC CTC GAC GAG CCC TGC GGC CTG GAC GCC GGC GCC GCC ACC Ala Pro Val Leu Asp Glu Pro Cys Gly Leu Asp Ala Gly Ala Ala Thr 515 520 525 530	1701
GCC GCC GCA GCA AGT GCC ACA GCG CCG TGC GCG TAGAAGACCT GGCACCCCA Ala Ala Ala Ser Ala Thr Ala Pro Cys Ala 535 540	1754
CGCGCCATGC ATGATTCGTG CGTGCTAGCT GTTGAAGGGA CGCCGGACAT TGAATGTGTA	1814
GATAGGGCAG CAGTGCAAGA CCGTAAGTAA AATTGATGAT GGGTTTGGTG ACAACATTTGA	1874
AGCCACTCT TTCCAGAATT TACGACCCGG ATAGGAGAAA CAGGGAAACT TTGCAGATCA	1934
CAACACAAGA TCTAGCCAGC CGGGGATCTG ATCTGATTTG CGCTGCTCG GACCACGGGT	1994
GCATGGGAGA CCAAGGAGGA AAACAAAAAA TAACAGAAC AGAGTGAGCA ATATTTGTGA	2054
TTGTAGCCAC GGGAAAGAGA GAGGAGTAAT TAGTAATTCA GATTTGTTTG CAGTAGCTCG	2114
GTGTTGGTGA CCAGATCATA GCCAACTAGG CTATTCTATT CTATTCTATT TTTGAAGATG	2174
ATTTTTC	2181

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATATATGGAT CCATGGAGGT GGGGACGTGG GCGGTGGTG

39

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ATATATGGAT CCATGGAAGT TGGTACTTGG GCTGTTGTTG TTTCTGCTGT TGCTGCTTAT

60

ATGGCTTGGT TTTGGAGAAT GTCTAGAGGT TTGAGAGGTC CAAGAGTTG GCCAGTTTG

120

GGTTCTTGC CAGGCCTGGT GCAGCACGCC

150

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleotide

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "reverse"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TATATAGAAT TCCTTCTACG CGCACGGCGC TGTGGCACTT GC

42

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1626 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1623
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATG GAA GTT GGT ACT TGG GCT GTT GTT TCT GCT GTT GCT GCT TAT
 Met Glu Val Gly Thr Trp Ala Val Val Val Ser Ala Val Ala Ala Tyr
 1 5 10 15

48

ATG GCT TGG TTT TGG AGA ATG TCT AGA CGT TTG AGA GGT CCA AGA GTT
 Met Ala Trp Phe Trp Arg Met Ser Arg Gly Leu Arg Gly Pro Arg Val
 20 25 30

96

TGG CCA GTT TTG GGT TCT TTG CCA GGC CTG GTG CAG CAC GCC GAG GAC
 Trp Pro Val Leu Gly Ser Leu Pro Gly Leu Val Gln His Ala Glu Asp
 35 40 45

144

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ATG CAC GAG TGG ATC GCC GGC AAC CTG CGC CGC GCG GGC GGC ACG TAC Met His Glu Trp Ile Ala Gly Asn Leu Arg Arg Ala Gly Gly Thr Tyr 50 55 60	192
CAG ACC TGC ATC TTC GCC GTG CCC GGG GTG GCG CGC CCC GGC GGC CTG Gln Thr Cys Ile Phe Ala Val Pro Gly Val Ala Arg Arg Gly Gly Leu 65 70 75 80	240
GTC ACC GTC ACC TGC GAC CCG CCC AAC CTG GAG CAC GTC CTG AAG GCG Val Thr Val Thr Cys Asp Pro Arg Asn Leu Glu His Val Leu Lys Ala 85 90 95	288
CGC TTC GAC AAC TAC CCC AAG GGC CCC TTC TGG CAC GGC GTC TTC CGG Arg Phe Asp Asn Tyr Pro Lys Gly Pro Phe Trp His Gly Val Phe Arg 100 105 110	336
GAC CTG CTC GGC GAC GGC ATC TTC AAT TCC GAC GGC GAC ACC TGG CTC Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Leu 115 120 125	384
GCG CAG CGC AAG ACC GCG CCG CTC GAG TTC ACC ACC CGC ACG CTC CGG Ala Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Arg Thr Leu Arg 130 135 140	432
ACG GCC ATG TCC CGC TGG GTC TCG CGC TCC ATC CAC GGC CGC CTC CTG Thr Ala Met Ser Arg Trp Val Ser Arg Ser Ile His Gly Arg Leu Leu 145 150 155 160	480
CCC ATC CTG GCC GAC GCG GCC AAG GGC AAG GCG CAG GTG GAT CTC CAG Pro Ile Leu Ala Asp Ala Ala Lys Gly Lys Ala Gln Val Asp Leu Gln 165 170 175	528
GAC CTC CTC CTC CGC CTC ACC TTC GAC AAC ATC TGC GGC CTG GCC TTC Asp Leu Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Ala Phe 180 185 190	576
GGC AAG GAC CCG GAG ACG CTC GCC CAG GGC CTG CCG GAG AAC GAG TTC Gly Lys Asp Pro Glu Thr Leu Ala Gln Gly Leu Pro Glu Asn Glu Phe 195 200 205	624
GCC TCC GCG TTC GAC CGC GCC ACC GAG GCC ACG CTC AAC CGC TTC ATC Ala Ser Ala Phe Asp Arg Ala Thr Glu Ala Thr Leu Asn Arg Phe Ile 210 215 220	672
TTC CCG GAG TTC CTG TGG CGC TGC AAA AAG TGG CTG GGC CTC CGC ATG Phe Pro Glu Phe Leu Trp Arg Cys Lys Lys Trp Leu Gly Leu Gly Met 225 230 235 240	720
GAG ACC ACG CTG ACC AGC AGC ATG GCC CAC GTC GAC CAG TAC CTC GCC Glu Thr Thr Leu Thr Ser Ser Met Ala His Val Asp Gln Tyr Leu Ala 245 250 255	768
GCC GTC ATC AAG AAG CGC AAG CTC GAG CTC GCC GGC AAC GGC AAA Ala Val Ile Lys Lys Arg Lys Leu Glu Leu Ala Ala Gly Asn Gly Lys 260 265 270	816
TGC GAC ACG GCG GCG ACG CAC GAC GAC CTG CTC TCC CGG TTC ATG CGG Cys Asp Thr Ala Ala Thr His Asp Asp Leu Leu Ser Arg Phe Met Arg 275 280 285	864
AAG GGT TCC TAC TCG GAC GAG TCG CTC CAG CAC GTG GCG CTC AAC TTC Lys Gly Ser Tyr Ser Asp Glu Ser Leu Gln His Val Ala Leu Asn Phe 290 295 300	912
ATC CTC GCC GGC CGC GAC ACC TCC TCC GTG GCG CTC TCC TGG TTC TTC Ile Leu Ala Gly Arg Asp Thr Ser Ser Val Ala Leu Ser Trp Phe Phe 305 310 315 320	960

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TGG CTC GTG TCC ACC CAC CCT GCG GTG GAG CGC AAG ATC GTG CGC GAG Trp Leu Val Ser Thr His Pro Ala Val Glu Arg Lys Ile Val Arg Glu 325 330 335	1008
CTC TGC TCC GTT CTC GCC GCG TCA CGG GGC GCC CAT GAC CCG GCA TTG Leu Cys Ser Val Leu Ala Ala Ser Arg Gly Ala His Asp Pro Ala Leu 340 345 350	1056
TGG CTG GCG GAG CCC TTC ACC TTC GAG GAG CTC GAC CGC CTG GTC TAC Trp Leu Ala Glu Pro Phe Thr Phe Glu Glu Leu Asp Arg Leu Val Tyr 355 360 365	1104
CTC AAG GCG GCG CTG TCG GAG ACC CTC CGC CTC TAC CCC TCC GTC CCC Leu Lys Ala Ala Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro 370 375 380	1152
GAG GAC TCC AAG CAC GTC GTC GCG GAC GAC TAC CTC CCC GAC GGC ACC Glu Asp Ser Lys His Val Val Ala Asp Asp Tyr Leu Pro Asp Gly Thr 385 390 395 400	1200
TTC GTG CCG GCC GGG TCG TCG GTC ACC TAC TCC ATA TAC TCG GCG GGG Phe Val Pro Ala Gly Ser Ser Val Thr Tyr Ser Ile Tyr Ser Ala Gly 405 410 415	1248
CGC ATG AAG GGG GTG TGG GGG GAG GAC TGC CTC GAG TTC CGG CCG GAG Arg Met Lys Gly Val Trp Gly Glu Asp Cys Leu Glu Phe Arg Pro Glu 420 425 430	1296
CGA TGG CTG TCG GCC GAC GGC ACC AAG TTC GAG CAG CAC GAC TCG TAC Arg Trp Leu Ser Ala Asp Gly Thr Lys Phe Glu Gln His Asp Ser Tyr 435 440 445	1344
AAG TTC GTG GCG TTC AAC GCC GGG CCG AGG GTG TGC CTG GGC AAG GAC Lys Phe Val Ala Phe Asn Ala Gly Pro Arg Val Leu Gly Lys Asp 450 455 460	1392
CTA GCC TAC CTG CAG ATG AAG AAC ATC GCC GGG AGC GTG CTG CTC CGG Leu Ala Tyr Leu Gln Met Lys Asn Ile Ala Gly Ser Val Leu Leu Arg 465 470 475 480	1440
CAC CGC CTG ACC GTG GCG CCG GGC CAC CGC GTG GAG CAG AAG ATG TCG His Arg Leu Thr Val Ala Pro Gly His Arg Val Glu Gln Lys Met Ser 485 490 495	1488
CTC ACG CTC TTC ATG AAG GGC GGG CTA CGG ATG GAG GTA CGT CCG CGC Leu Thr Leu Phe Met Lys Gly Gly Leu Arg Met Glu Val Arg Pro Arg 500 505 510	1536
GAC CTC GCC CCC GTG CTC GAC GAG CCC TGC GGC CTG GAC GGC GGC GCC Asp Leu Ala Pro Val Leu Asp Glu Pro Cys Gly Leu Asp Ala Gly Ala 515 520 525	1584
GCC ACC GCC GCC GCA GCA AGT GCC ACA GCG CCG TGC GCG TAG Ala Thr Ala Ala Ala Ser Ala Thr Ala Pro Cys Ala 530 535 540	1626